

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 22, 2000, 13:41:24, Search time 12.1 seconds
(without alignments)
64,172 Million cell updates/sec

Title: US-09-386-591-23

Perfect score: 134

Sequence: 1 KINGSLIGHTMPCPFRFIVFLQSLIS 26

Scoring table: BUSUM62

Searched: 22223 seqs 2265246 residues

Database: SwissProt231*

Word size: 0

Number of hits that pass the threshold: 82223

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	IE	ID	Description
1	134	100.0	493	1	CE1P_HUMAN	Plas97 homo sapien
2	134	100.0	493	1	CE1P_MACEA	P47896 maceca fasc
3	132	99.6	239	1	CE1P_MESAU	P25944 mesocricetu
4	117	87.3	467	1	CE1P_PABIT	P22847 cryptotagus
5	52	23.9	317	1	YCAC_HAELN	C57121 haemophilus
6	50	37.3	311	1	YDAQ_ECOLI	P76055 escherichia
7	48	35.8	348	1	AROH_EAGLI	P06447 escherichia
8	46	34.7	377	1	QDSQ_HWSEA	P05158 hemigrapsus
9	46	34.3	422	1	AP17_CABEL	P25522 caenorhabdi
10	46	34.3	423	1	PR11_PABIT	P34358 pabityronem
11	45.5	34.0	1216	1	YMW2_CABEL	P34504 caenorhabdi
12	45	33.5	274	1	YF1F_AEPEC	P26685 african swi
13	44.5	33.2	2290	1	P0LG_EMAC	P33334 escherichia
14	44.5	33.2	2290	1	P0LG_PVAVE	P17593 escherichia
15	44.5	33.2	2290	1	P0LG_PVAVE	P17593 escherichia
16	44.5	33.2	2290	1	P0LG_PVAVE	P17593 escherichia
17	44	32.9	429	1	AP50_DYCTI	P24767 dictyostel
18	44	32.9	472	1	Q001_ASAAT	P12060 arabidopsi
19	44	32.5	310	1	YB15_NYVAL	P31133 escherichia
20	42.5	32.5	340	1	YF1F_VIBRI	P24447 vibrio chol
21	42	32.1	423	1	AP47_MORSE	P35526 mus musculu
22	42	32.1	410	1	YFMC_SALTY	P26319 salmonella
23	42	32.1	487	1	YF1F_AEPEC	P26319 salmonella
24	42	32.1	487	1	YF1F_AEPEC	P26319 salmonella
25	42	32.1	487	1	YF1F_AEPEC	P26319 salmonella
26	42	32.1	487	1	YF1F_AEPEC	P26319 salmonella
27	42	32.1	487	1	YF1F_AEPEC	P26319 salmonella
28	42	32.1	487	1	YF1F_AEPEC	P26319 salmonella
29	42	32.1	487	1	YF1F_AEPEC	P26319 salmonella
30	42	32.1	487	1	YF1F_AEPEC	P26319 salmonella
31	42	32.1	487	1	YF1F_AEPEC	P26319 salmonella
32	42	32.1	487	1	YF1F_AEPEC	P26319 salmonella
33	41.5	31.0	721	1	YF1F_AEPEC	P26319 salmonella
34	41.5	31.0	721	1	YF1F_AEPEC	P26319 salmonella
35	41.5	31.0	721	1	YF1F_AEPEC	P26319 salmonella
36	41	30.6	569	1	Q001_HUMAN	P15511 homo sapien
37	41	30.6	569	1	Q001_HUMAN	P15511 homo sapien
38	41	30.6	569	1	Q001_HUMAN	P15511 homo sapien
39	41	30.6	569	1	Q001_HUMAN	P15511 homo sapien

1 41 30.6 577 1 SVI_HELPY
2 41 30.6 592 1 SVI_MVCH
3 41 30.6 635 1 SVI_PICPE
4 41 30.6 255 1 GPP3_METTH
5 41 30.6 386 1 YS74_MTCIG
6 41 30.6 404 1 YF1F_HALIN
7 41 30.6 404 1 YF1F_HALIN

ALIGNMENTS

RESULT 1
CE1P_HUMAN
10 CE1P_HUMAN STANDARD; PRI: 493 AA.
AC P11597: 013987: 013988:
01 OCT-1989 (Rel. 12, Created:
01-OCT-1989 (Rel. 12, Last sequence update)
11 YF1F_HALIN (Rel. 12, Last sequence update)
12 YF1F_HALIN (Rel. 12, Last sequence update)
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98 YF1F_HALIN (Rel. 12, Last sequence update)
99 YF1F_HALIN (Rel. 12, Last sequence update)
100 YF1F_HALIN (Rel. 12, Last sequence update)

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EMBL: M32994; AAA51978.1: JOINED.
R K EMBL: M32995; AAA51978.1: JOINED.
K R EMBL: M32996; AAA51978.1: JOINED.
K R EMBL: M32997; AAA51978.1: JOINED.
K R EMBL: M83573; AAB59388.1: -.
K R PIR: A25943; A25941
R MM: 118470; .
R PRSITE: PS00400; LRP_RPI_CETP: 1.
R PFAM: PF0273; LRP_RPI_CETP: 1.
W lipid transport; Cholesterol metabolism; Glycoprotein; Signal;
W Atherosclerosis; Disease mutation.
T SIGNAL: 1 17 CHOLESTERYL ESTER TRANSFER PROTEIN.
T CHAIN: 18 493 POTENTIAL.
T CARBOHYD: 105 105 POTENTIAL.
T CARBOXYD: 257 257 POTENTIAL.
T CARBOHYD: 358 358 POTENTIAL.
T CARBOHYD: 413 413 POTENTIAL.
T VARIANT: 459 459 /FTIG-VAE2004172.
I C-FLUOCT 422 422 I -> V (IN REF. 2).
I C-FLUOCT 251 310 MISSING (IN REF. 3).
T SEQUENCE 493 AA: 54770 MW: 5949608 GRG32:
Query Match 100.0% Score 134 DB 1 Length 493:
Best local Similarity 100.0% Proc No. 2.5e-14
Matches 26 Conservative 0 Mismatches 0 Indels 0 Gaps 0:
QY 1 RDGFLLMDPGFPEHLVDFLOSLS 26
DB 111111111111111111111
498 RDGFLLMDPGFPEHLVDFLOSLS 493
RESULT 2
CETP_MAFRA STANDARD: FRG: 493 AA.
AC FAY896:
DT 01-FEB-1996 (Ref. 43, Created)
DI 01-FEB-1996 (Ref. 43, Last sequence update)
DI 15-DEC-1998 (Ref. 37, Last annotation update)
DE CH-ESTERYL ESTER TRANSFER PROTEIN DEFECTIVE (LPID TRANSFER PROTEIN
GN CETP
OS Macaca fascicularis (Orangutan macaque) (Cynomolgus monkey).
OC Eukaryota Metazoa Chordata Craniata Vertebrata Mammalia
OC Etheria Primates Catarrhini Cercopithecoidea Cercopithecinae
OC Macaca.
RN [1]
RS SEQUENCE FROM N.A.
RX MEDLINE: 92041355
FA PAPE M.E., REHBERG P.F., MAROTTA K.R., MELCHIOR G.W.:
BT "Molecular cloning, sequence, and expression of cynomolgus monkey
BT "cholesterol ester transfer protein, its large correlation between
BT hepatic cholesterol ester transfer protein mRNA levels and plasma
BT high density lipoprotein levels."
BT Arterioscler Thromb 11:1759-1771(1991).
RL ALLELIC FORMS OF THE HUMAN GENES FOR AN EXTREMELY HYDROPHOBIC PROTEIN INVOLVED IN THE
CC (-) FUNCTION: CETP IS AN EXTREMELY HYDROPHOBIC PROTEIN INVOLVED IN THE TRANSPORT
CC OF CHOLESTEROL.
CC (-) SUBCELLULAR LOCATION: EXTRA-CELLULAR.
CC (-) TISSUE SPECIFICITY: PLASMA. CONCENTRATION ACTIVITY IN THE LIVER.
CC (-) SIMILARITY: REFERENCE TO THE REF. 14: CETP FAMILY
CC This SWISS-Prot entry is copyright © It is produced through a collaboration
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CC or send an email to license@ebi.ac.uk).
DR EMBL M86443; AAA46840.1: .
DR DDB PS00400; LRP_RPI_CETP: 1

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PFAM: PF01273; LRP_RFL_CETP; 1
Lipid transport; Cholesterol
SYGNAL 1 17
CHAIN 18 493
CATABOLISM 59 59
POTENTIAL 59 105
POTENTIAL 105 105
POTENTIAL 105 257
POTENTIAL 257 458
POTENTIAL 458 558
POTENTIAL 558 613
POTENTIAL 613 414
SEQUENCE 493 AA; 54743 MW; 4PM7E27 CDS42;
Query Match: 100.0%; Score 145; DB 1; Length 493
Post Local Similarity 100.0%; Pred. No. 2, 50-14;
Matches 26; Conservative 0; Mismatches 0; Indels 1; Gaps 0;
O9 1 RUSFLLQMDGFGPHHLLVDFLQSL 26
DE 468 RUSFLLQMDGFGPHHLLVDFLQSL 494
RESULT 2
CF.P.F.MESAD
IL CETP-MESAO STANDARD; PRI: 28% AA.
DI 01-MAY-1992 (Rel. 22, Created)
DI 01-MAY-1992 (Rel. 22, Last sequence update)
DI 01-MAY-1992 (Rel. 25, Last annotation update)
DI 01-NOV-1997 (Rel. 25, Last annotation update)
DI CHOLESTERYL ESTER TRANSFER PROTEIN (LIPID TRANSFER PROTEIN 1)
DE CHOLESTERYL ESTER TRANSFER PROTEIN (LIPID TRANSFER PROTEIN 1)
DE (FRAGMENT).
DE CETP.
DE Mesocricetus auratus (Golden hamster).
DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
DE Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mesocricetinae.
DE (1)
DE SEQUENCE FROM N.A.
DE MEDLINE: 91154277.
DE JIANG X C., MOULIN P., QUINEE E., GILLBERG L., YANDEB L.,
DE AGELLON L.B., COMPTON D., SCHNITZER-POLKOFF P., LALLA A. &
DE "Mammalian adipose tissue and muscle are major sources of LRP-1
DE transfer protein mRNA."
DE J. Biol. Chem. 266:6931-6939(1991).
DE FUNCTION: CETP IS AN EXTREMELY HYDROPHOBIC PROTEIN INVOLVED IN THE
DE TRANSFER OF INSOLUBLE CHOLESTERYL ESTERS IN THE REVERSE TRANSFER
DE OF CHOLESTEROL.
DE SOURCE/CELLULAR LOCATION: EXTRACELLULAR.
DE TISSUE SPECIFICITY: PLASMA.
DE SIMILARITY: BELONGS TO THE LRP-1 FAMILY.
DE THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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DE modified and the statement is not removed. Usage by any other means
DE without requires a license agreement (See http://www.ebi.ac.uk/ebis/
DE or send an email to license@ebi.ac.uk)
DE EMBL: M63992; AAA37066.1;
DE PIR: A38700; A38700.
DE PROSITE: PS00400; LRP_RFL_CETP; 1.
DE PFAM: PF01273; LRP_RFL_CETP; 1.
DE Lipid transport; Cholesterol metabolism; Glycolipids.
DE 4_170.
DE 53 53 POTENTIAL.
DE 53 53
DE 284 AA; 32430 MW; RA74EF74 CDS42;
DE SHORER.
Query Match: 97.8%; Score 141; DB 1; Length 284
Post Local Similarity 95.2%; Pred. No. 40-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
O9 1 RUSFLLQMDGFGPHHLLVDFLQSL 26
DE 468 RUSFLLQMDGFGPHHLLVDFLQSL 494

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[illegible][illegible]

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Query Match: 45.8%; Score: 48; DB: 1; Length: 48;
Best local similarity: 66.7%; Pred. No. 4, 6;
Matches: 8; Conservative: 2; Mismatches: 2; Gaps: 0;
: 10 DFGFPERLLVDF 2;
: 1 111111
: 95A FDFLPERLLVDF 265

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[illegible]

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RX      REMARK: G116-2744.
RA      TAAAGACATGATGAAGTCTAATGGGCAATC
RC      "Analysis of products of the Escherichia coli genomic locus and
RI      regulation of its expression." A applicable procedure for genetic
RT      analysis of other microorganisms."
RL      Biosci Biotechnol Biochem 58:117-120(1994).
RM      - SIMILARITY STRING TO HYPHENATED PII 371
RC      -----
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CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (see http://www.ebi.ac.uk/db/eng/eng/
CC      or send an email to license@sb.sib.ch)
CC      -----
CC      ENRL: AE000242; AN:74426.1;
CC      ENSL: D21134; PAAD04475.1;
CC      EC_GENE: E013457; YUAC
CC      PRAM: PF01171; UPF0021; 1
CC      uncharacterized protein
CC      CONFLICT 11 11 F -- A VIKR...
CC      SEQUENCE 313 AA; 35561 MW; 138B5071 CRC32;
SU

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	RESULT	7	
	ARCH_EPOCH	1	
	ARCH_EPOCH	1	STANDARD:
	PID	9887	PID: 648 AA.
	DATE	21-JUL-1986	(Rel. 01, Created)
	DATE	01-MAR-1992	(Rel. 21, Last sequence update)
	DATE	01-NOV-1997	(Rel. 35, Last annotation update)
	DE	EPHSPB-2-DEHYDRO-3-DEXYHEPTANATE ALLOLASE, TRP SINGULIF	
	DE	(EC 4.1.2.15), (FBI-SECH 2 F1-2-3) ANTHRAQUINONE ALLOLASE (NAP	
	DE	SYNTHETAS) (4-DEXY D ARABIN--HEXITOLONATE 7-PHOSPHATE SYNTHASE).	
	GN	Arch.	
	ES	Escherichia coli.	
	Bacterial	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;	
	Escherichia	Escherichia.	

1.1. SEQUENCE FROM N.A.
1.2. MEDLINE: 6323737.
1.3. HEDSON G.S., BELLOS P., DAVLISH R.P.:
1.4. "Two promoters control the archi gene of *Escherichia coli*":
1.5. Gene 102:87-91(1991).
1.6. 1.1. SEQUENCE FROM N.A.
1.7. MEDLINE: 84054867.
1.8. RAY J.M., VANDERFSKY C., BAUDERLE R.:
1.9. "Mutational analysis of the catalytic and feedback sites of the
1.10. tryptophan synthetase 8-hydroxy-5-arabino-hydroxymethyl-7-phosphate
1.11. synthase of *Escherichia coli*":
1.12. J. Bacteriol. 170:5500-5509(1988).
1.13. 1.1. SEQUENCE FROM N.A.
1.14. MEDLINE: 8494812 / 601655.
1.15. MEDLINE: 87426417.
1.16. GALLAGHER P.W., PINKERT J. III, RUDCH C.A., PERNA N.L., RUSLAND V.,
1.17. RILEY M., COLLAPARVIDES J., SHANEN F.D., ROBE L.A., MATHEN C.F.,
1.18. BREWER J., DAVIS R.W., KIRKLAND H.A., GORDEN M.A., BUSE D.L.:
1.19. "The complete genome sequence of *Escherichia coli* K-12":
1.20. Science 277:1243-1247(1997).
1.21. 1.1. SEQUENCE FROM N.A.
1.22. MEDLINE: 87426417.

